

CCGGCAAAAG CAGCTCCGAC CCCCTGCAAA CCCTTCACC TCCAACTGCA ATTGATAGAG TTATCCAACC AGCAGGTTGA GACTGAGAGC CTAAGAAAGA CTTACAGTAA ATGTGTCCCA GTTGGAGTCA AGACATATAA TTGTGCTGTA TAGATACCAT AATTGGCATT CTGTGGTTAT AAAA CTAAAAGGAG AGTCAGATTT ATCTGCCGGA AGAAAATGTG TTAAGAATCA TATAGAAATC CCTGCTGCAG TCAACAAAGG TGGCATATGA AAGATAATGC ATAACGACTA CTATCGTCGC CAAATCATGC AGCAAATATC TGCTCTATGT AATATGGATA AAAAAAAA CTGCCACACC AAGGGCCTTT AACCGGTTGC GAGCGGAAGT CGTTTTCCGG GTGTGAGGGG TTGATGAAAA TACTCAGTGG TGACAGCATG CGCCCTTCC ATTAAGGGTA ATGGCTTAAT AGACAAAGAG TAAGCTTTAC GAAAACAGCA ATTGAGAAAG TGATGGGCTG ACTTGGGCTA GCTAAAAAA GCCATGAACA TCCTTTTATC GAGTCCAGAG ACTGCTGAGG CCTCCTCT GGCCTTCCTC TTCCCATTCC TTCAAGAAAT GTATTGAACC ATAGICCGAI ACTCTTTTT ATCAAATTTG CTCCTGGAGC ATGGCAGAAG TGCAGAAGAC ATTATTAAA GAAGGAATGC TGTCTGTGTG TTCACCAGAT AACTTCAGTT TTCACAAATA CGCCTACGTG GCTACCTCCA CGTAAAGCGC GTCAGTGCC TGGATCATG TCCAGTTGAA CAATTTCCAG TGTTGCTATC SAAAATATCC TCTGTGTTTG TCCTGTCAAA ATGGAGAATT TAAAGGAGCC TGAAGATGTC ATGAGCCTCA GCTGAATAAA TCAATTTCT CTAAGATTAC GGCTTAACTT 51 151 51 01 451 551 601 651 51 251 301 501 01 801 201 51 901

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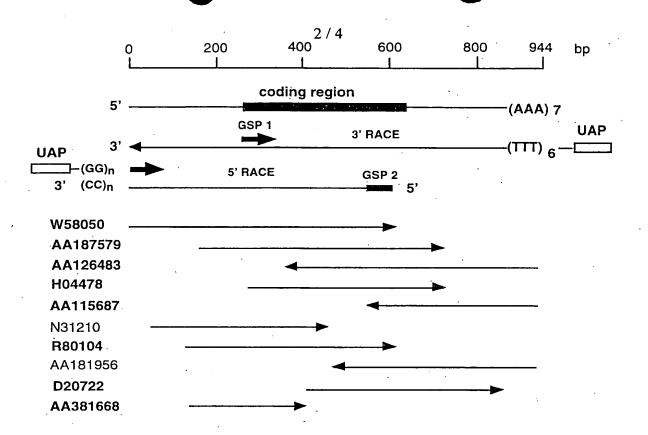


Fig. 2

Glycosylation Site

Tyr Phosphorylation Site

TLRLLHKYPF ILPHQQVDKG EQFPGIEPWL NQIMPKKDPV VIKGIKNQLL MFKKFDEKEN VSNCIOLKTS

GVMKMSAEDI AAVDTIVAIM AEGKQHALCV FROREGPEYP ILTVNGELLF LTSPGAKLYP KIVRCHEHIE AIKANIMCPG 101 51

HMKTYK NIHYLNDGLW EKVNKGIGIE 151

PKC Phosphorylation Sites

CK2 Phosphorylation Site

51 $_{239}$ KEN.RTCLSQLLDIMKSMRN.LVKKYE..PPRSEEVAVLKQ..K $_{277}$ 8 KENVSNCIQLKTSVIKGIKNQLIEQFPGIEPWLNQIMPKKDPVK Cyclin H

Cyclin H 278LERCHS.AE.LALN288 52 IVRCHEHIEILTVN

CCGGCAAAAG CCCCTGCAAA ATGTGTCCAG ATTGGCATTG TGTGGTTATG GACTGAGAGC ATTGATAGAG CTAAGAAAGA CTTACAGTAA TTATCCAACC AGCAGGTTGA CAGCTCCGAC CCCCTTCACC TCCAACTGCA AGATACCATT GACATATAAA TGTGCTGTAT TIGGAGICAI AAA CTAAAAGGAG AGTCAGATTT ATCTGCCGGA CTATCGTCGC AGAAAATGTG ATAACGACTA TTAAGAATCA CTGCCACACC AGCAAATATC CTGCTGCAGT CAAATCAIGC TATAGAAATC AAGGGCCTTT GCTCTATGTG CAACAAAGGA GGCATATGAA ATATGGATAT AGATAATGCC AAAAAAAAA TACTCAGTGG AACCGGTTGC GAGCGGAAGT CGTTTTCCGG GTGTGAGGGG TTGATGAAAA ATTAAGGGTA AGACAAAGAG GACAGCATGA CGGCCCTTCC ATGGCTTAAT GCCATGAACA TCCTTTTATC AAGCTTTACC AAAACAGCAT CTTGGGCTAA CTAAAAAAA TTGAGAAAGT GATGGGCTGT ACTGCTGAGG GAGICCAGAG GGCCTTCCTC GTCTGTGTGT TCACCAGATG TICCCATICC TTCAAGAAAT ATCAAATTTG TGGCAGAAGG AAGGAATGCA GGCTGGCTCT AACTICAGII GTATTGAACC TTCACAAATA TCCTGGAGCT GCAGAAGACA ATAGTCCGAT ACTCTTTTT TTATTTAAAT GCTACCTCCA CGCCTACGTG CGTAAAGCGC TTGGATCATG GTCAGTGCC TCCAGTTGAA CAATTTCCAG **rga**gcctcag TCAATTTCT TCCTGTCAAA ATGGAGAATT CTAAGATTAC TAAAGGAGCC GCTTAACTTC STIGCTAICA SAAGATGTCT AAAATATCCA CTGTGTTTGT CTGAATAAAT 51 251 351 401 51 201 301 601 701 751 851 901 501 551 651 801

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